ORTHOLOGUES YEAST GENES ASSOCIATED WITH GLYCEROL TRANSPORT AND METABOLISM

Neves, L, Oliveira, R., Lucas, C.

Centro de Biologia da Universidade do Minho (CB-UM) / Dep. de Biologia, Universidade do Minho

Campus de Gualtar, 4710-057 Braga, Portugal

Glycerol, besides acting as compatible solute, accumulated by *S. cerevisiae* to counteract the low a_w stress environments, is a key compound in the regulation of multiple metabolic pathways. Most of the genes involved in glycerol consumption and production are now available for this yeast. Furthermore, three genes had been described as involved in glycerol uptake as well as export, respectively, *GUP1*/*2*[1] and *FPS1*[23]. Altogether, these genes regulate intracellular glycerol levels in a way not yet completely unveiled. Some of these mechanisms, like the stimulation of glycerol production and accumulation under stress growth conditions and the presence of constituvely active transport for glycerol, are common to a series of other yeasts[4]. Being so, we decided to search for some of the genes from glycerol uptake and metabolism in some of those yeasts. We began using the partial genome sequencing available for several yeasts from the Génolevures Program. Further ahead we included *Candida albicans* from Stanford Genome Sequencing Data Base. Our search focused on *GUP1*/*2*, *FPS1*, *GPD1/2* (glycerol 3-P dehydrogenase) and *GUT1* (glycerol kinase) genes. From this search we choosed the sequences with higher similarity, which were present in *Candida tropicalis, Kluveryomyces marxianus*, *Kluveryomyces lactis*, *Kluveryomyces thermotolerans*, *Pichia angusta*, *Pichia sorbitophila* and *Zigossacharomyces rouxii*, besides *Candida albicans*. The entire sequences of the genes were obtained using standard procedures, like primer walking sequencing and RACE (rapid amplification of cDNA ends). Genes were obtained by PCR and complementation analysis was done. Sequences were used to create/enlarge gene families, to explore the evolutionary relationship of these species and to establish the putative relation between sequence and function.

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[1] Holst *et al* (2000). Molecular Microbiology, 37: 108-124
[2] M. Tamás *et al* (1999) Molecular Microbiology, 31: 1087-1104
[3] M. Tamás *et al* (2000) FEBS Lett 21, 472: 159-18
[4] Lages & Lucas (1997). Bioquim Biophys Acta, 1322: 8-18